

# GENETIC RESPONSE AND INBREEDING IN SUB-POPULATION MATING SYSTEM FOR DAIRY CATTLE

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## SUMMARY

A closed nucleus dairy cattle population with multiple ovulation and embryo transfer (MOET) was stochastically simulated over 10 generations. Four mating designs were examined to identify the mating system which achieves a balance of genetic response and inbreeding in dairy herds. A population was divided into two sub-populations in designs 2, 3 and 4. Mating was independently carried out within each sub-population in design 2, and mating was carried out between two sub-populations in every other generation in designs 3 and 4. Design 1 gave the largest genetic response at high provability with a relatively high rate of inbreeding. The average annual rate of inbreeding in designs 3 and 4 were very small, and these results indicated the sub-population mating system was effective to suppress the increase of inbreeding. Relative inbreeding to response ratio (RIRR) in design 4 was the smallest, and the mating system adopted in design 4 would be suitable to achieve a balance of genetic response and inbreeding.

**Keywords:** MOET, genetic response, inbreeding, mating design

## INTRODUCTION

Recently, multiple ovulation and embryo transfer (MOET) technique has been widely adopted in breeding schemes of dairy cattle population. MOET can be useful in a relatively small population, but it is difficult to avoid the increase of inbreeding rates. Recent research has focused on a technique to achieve maximum genetic gain and limit inbreeding rates at the same time. Luo *et al.* (1995) studied on the feasibility of controlling inbreeding in several cases. Their results indicated the importance of incorporating progeny testing into MOET schemes for values of reducing inbreeding while maintaining genetic progress. Leitch *et al.* (1994,1995) reported on the effect of different selection methods and mating designs on genetic response and inbreeding.

The objectives of this study were to consider alternative mating designs in sub-population systems to offer a balance of genetic response and inbreeding.

## MATERIALS AND METHODS

The base population for the simulation consisted of 200 animals. The objective trait was milk yield assumed to have a mean 7325.7 kg, genetic standard deviation of 680.0 kg and heritability of 0.25 in the base population. Ten bulls and thirty donor heifers were selected and there were 60 mating each generation. Each heifer had two equal chances to mate. Males and females were assumed capable of breeding at 12 months of age. The number of transferable

embryos collected per flush and donor heifer was obtained from a Poisson distribution with mean 6.0. The proportion of transferred embryos resulting in a live calf was 50 %. Estimated breeding values of animals were calculated from the selection index theory. Index weights were calculated using records from cows being equal or larger than 0.25 additive relationship with the animal to be evaluated. Figure 1 indicates four mating designs considered in this study. Design 1 did not adopt a sub-population system. In designs 2, 3 and 4, the population was divided into two sub-populations. Five bulls and fifteen donor heifers were selected in each sub-population for each generation. Mating was independently carried out within each sub-population in design 2. In designs 3 and 4, mating between different sub-populations was carried out in every other generation. Animals resulted from the mating between different sub-populations belonged to dam's sub-population in design 3. On the other hand, males and females produced by mating between different sub-populations belonged to sire's and dam's sub-population, respectively. Annual rates of inbreeding were calculated using the equation of Falconer (1989). The relative inbreeding to response ratio (RIRR) was calculated to evaluate mating designs by method of Leitch *et al.* (1994, 1995). Simulation was carried out for 10 generations. Each of the four mating designs was stochastically simulated fifty times.

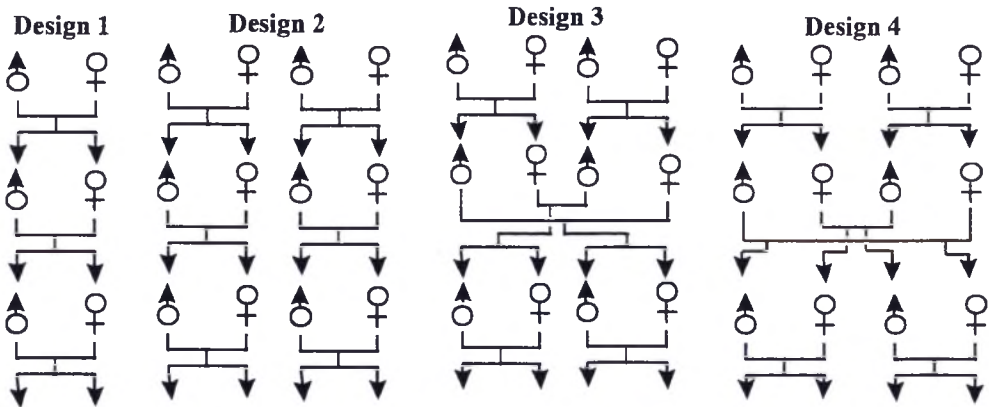


Figure 1. Mating design.

## RESULTS AND DISCUSSION

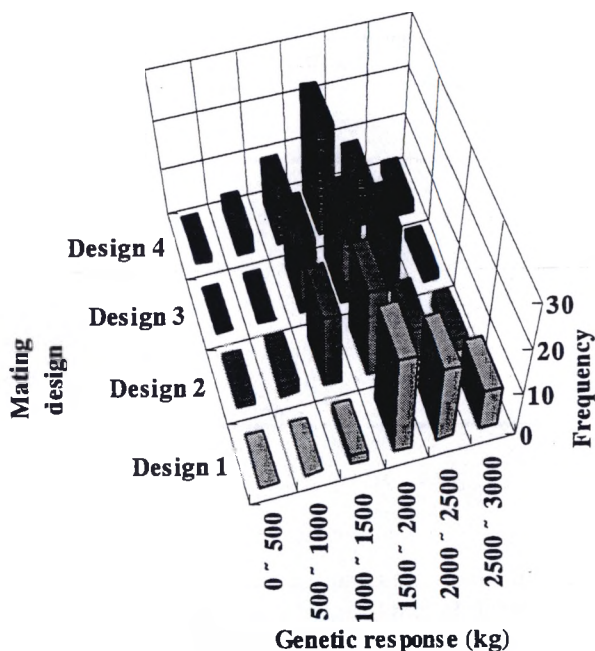
Average of population size, generation interval, true breeding value, inbreeding coefficient and accuracy of selection in tenth generation are presented in Table 1. Population size and generation interval were similar in all designs. True breeding value in design 1 was the largest and the smallest in design 4. True breeding value in designs 2 and 3 were similar to design 4. True breeding value in design 1 was about 1.2 times as large as the ones of other designs. The largest genetic response in design 1 indicated the effect of population size on genetic improvement. Inbreeding coefficient was the smallest in design 4 and the largest in design 2. In design 2, mating was independently carried out within each sub-population, and it was

reasonable to consider that there were two independent populations which were half of the population size in design 1.

**Table 1. Simulated average of population size, generation interval, true breeding value, inbreeding coefficient and accuracy of selection in tenth generation**

Item	Mating design			
	Design 1	Design 2	Design 3	Design 4
Population size	179.7	179.2	179.2	179.2
Generation interval (month)	22.0	21.9	21.9	21.9
True breeding value (kg) <sup>A</sup>	2041.6	1673.4	1728.4	1668.5
Inbreeding coefficient (%)	34.9	47.9	28.5	25.5
Accuracy of prediction	0.72	0.71	0.66	0.67

<sup>A</sup>True breeding value was a deviation from mean (7325.7 kg) in base population.



**Figure 2. Genetic response after 10 generations in four mating designs.**

About 20 cases out of 50 replications gave genetic responses of 1500 to 2000 kg in all designs (Figure 2). Especially, genetic responses of 23 cases of design 4 were in the range of 1500 to 2000 kg, and this frequency was 46 % of total. The second highest frequencies were in range of 1000 to 1500 kg or 2000 to 2500 kg in designs 2, 3 and 4. In design 1, however, only one case out of 50 replications had less than 1500 kg genetic response. This result indicated that design 1 could offer larger genetic responses at high provability. Table 2 indicated average annual rates of genetic response and percentage inbreeding and relative inbreeding to response ratio. The average annual rate of genetic response ( $\Delta R$ ) in design 1 was 111.5 kg / year and was the largest in four mating designs. Also, standard deviation of  $\Delta R$  was the smallest in design 1, and this result supported the consideration for design 1 in Figure 2. The small rates of percentage inbreeding ( $\Delta F$ ) in designs 3 and 4 indicated that mating between sub-populations was effective to suppress the increase of inbreeding. Relative inbreeding to response rate (RIRR) was the smallest (0.461) in design 4. In conclusion, design 1 was suitable to achieve larger annual rate of genetic response ignoring the increase of inbreeding. If a balance of genetic response and inbreeding should be needed, design 4 should be adopted in a breeding program.

**Table 2. Simulated average annual rates of genetic response (R) in real units and percentage inbreeding (F) and relative inbreeding to response ratios (RIRR).**

Item	Mating design			
	Design 1	Design 2	Design 3	Design 4
$\Delta R$ (kg / year)	111.5 (21.67) <sup>A</sup>	91.9 (26.52)	94.9 (25.32)	91.6 (25.51)
$\Delta F$	2.287 (0.409)	3.434 (0.387)	1.652 (0.213)	1.577 (0.220)
RIRR	0.549 <sup>B</sup>	1.000	0.466	0.461

<sup>A</sup>Standard deviation.

<sup>B</sup>RIRR = (2.287 / 3.434) / (111.5 / 91.9) = 0.549.

## REFERENCES

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